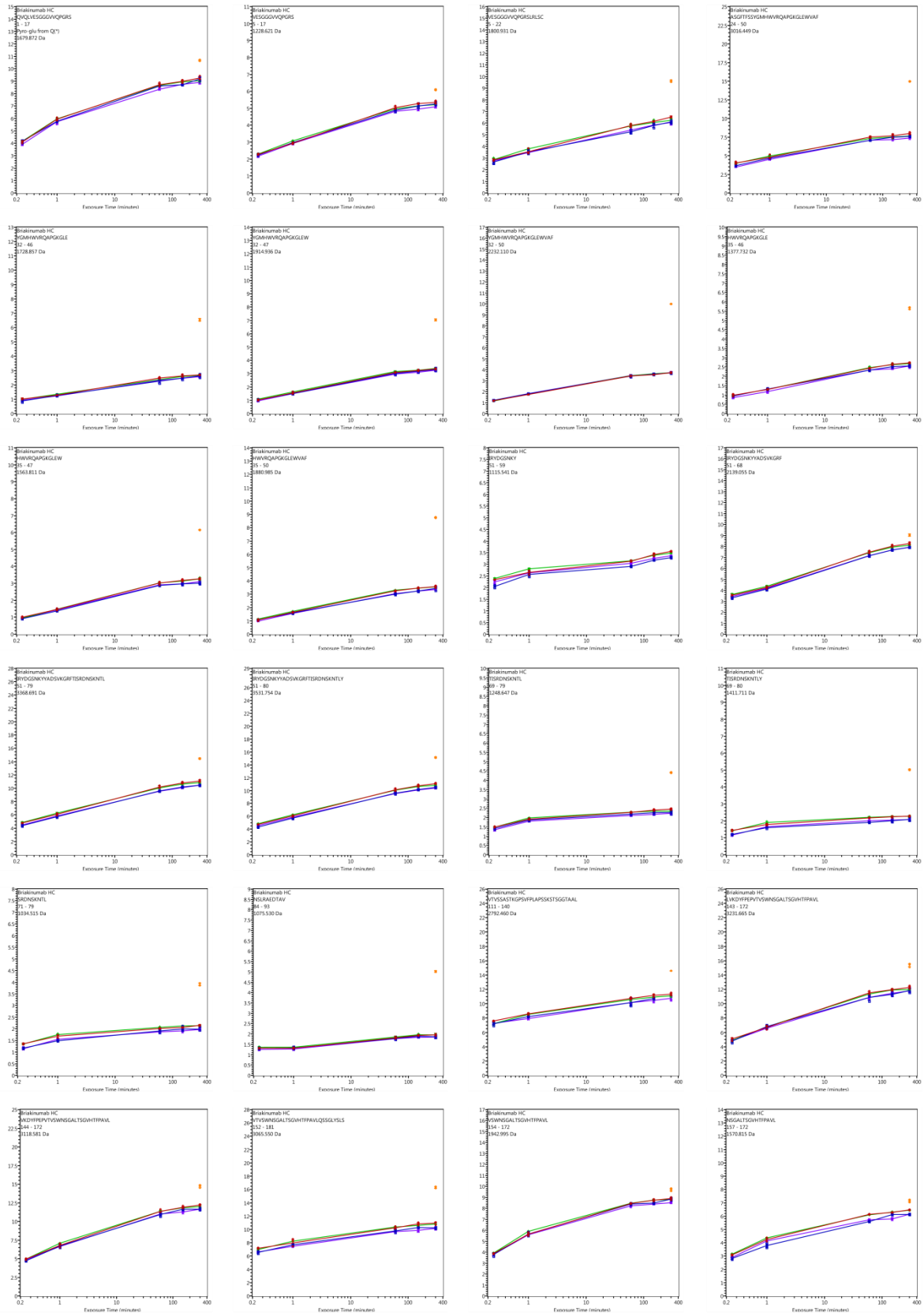
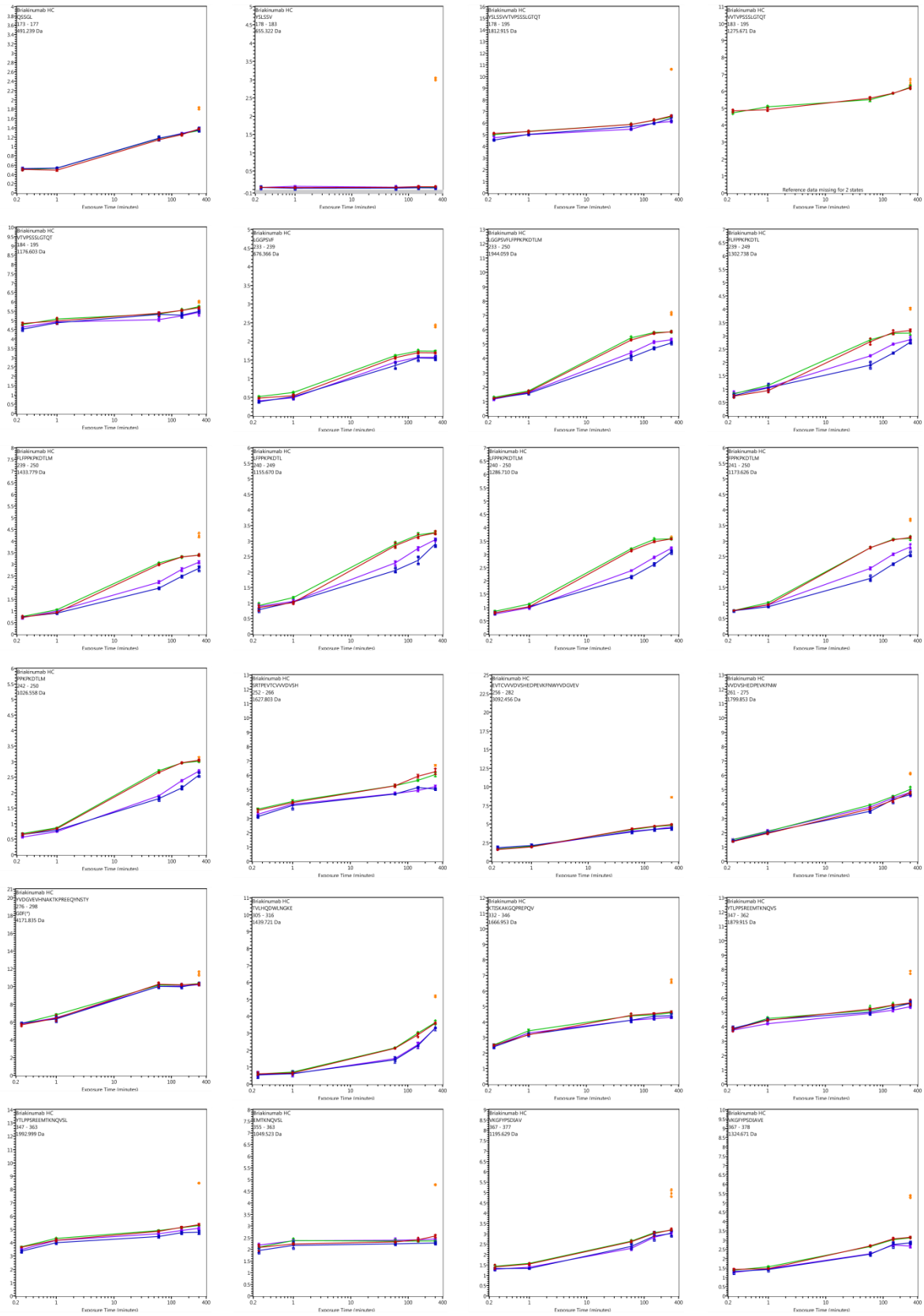
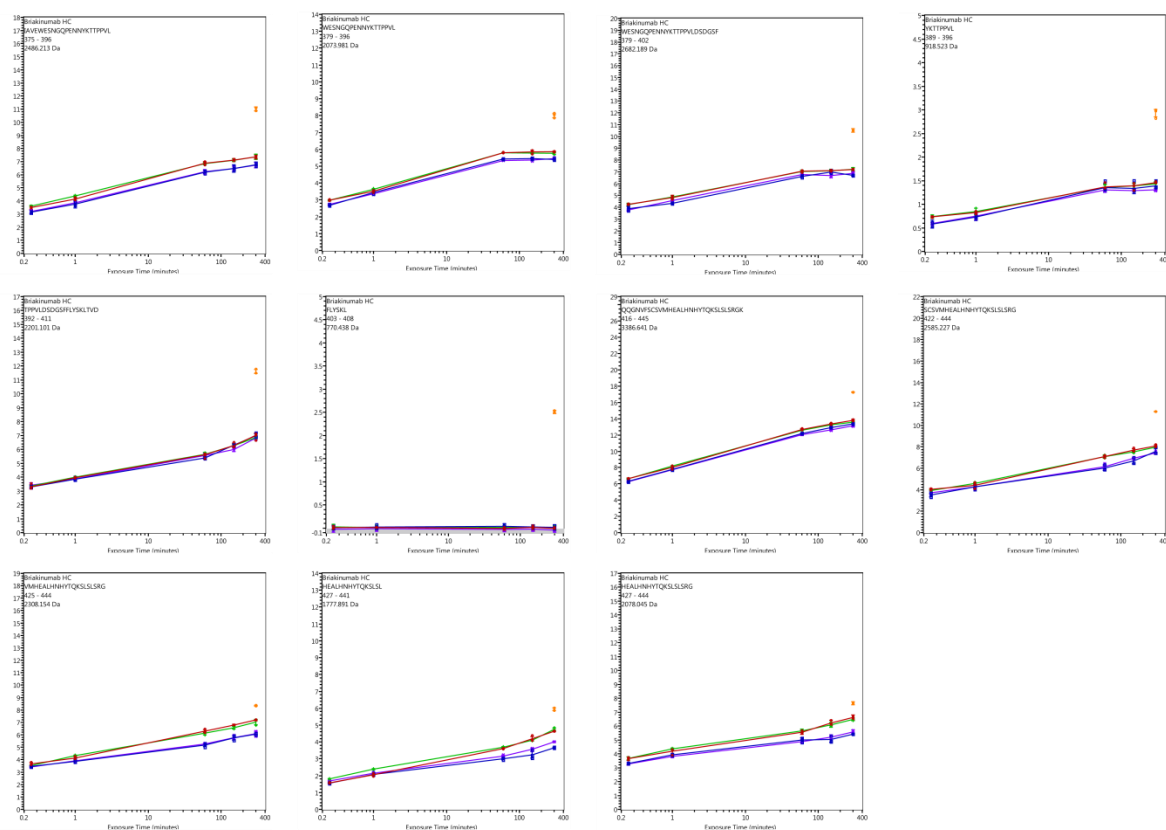


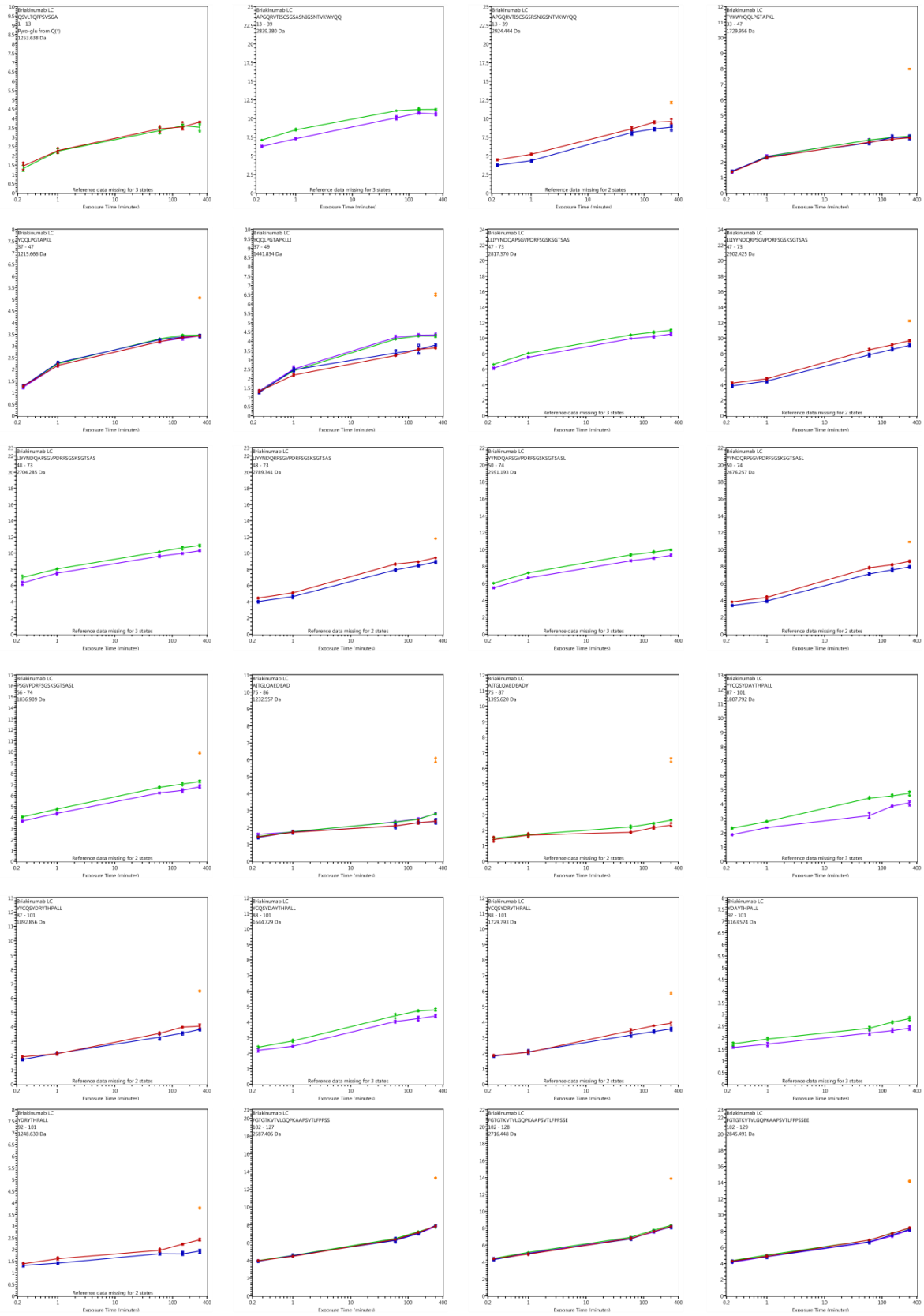
## **Supplemental information**

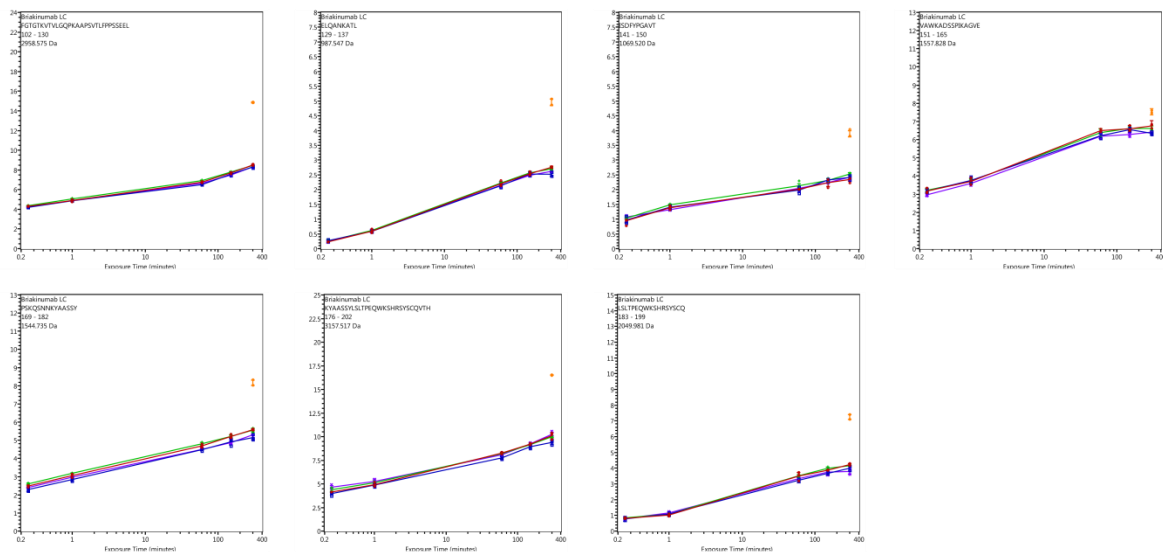






**Figure S1.** Deuterium uptake plots of heavy chain briakinumab and the briakinumab variant peptides. Deuterium incorporation of unbound briakinumab (red), FcRn-bound briakinumab (blue), unbound briakinumab variant (green), FcRn-bound briakinumab variant (purple) was determined in triplicate experiments at 15 s, 1 min, 1 h, 2.5 h and 5h and plotted with 1x standard deviation (in most cases the SD was lower than the size of the data point marker). The 90 % D<sub>2</sub>O control is shown in orange at the last time point.

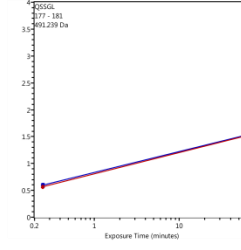
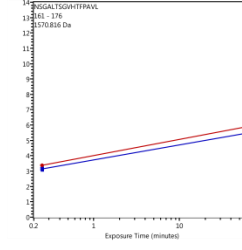
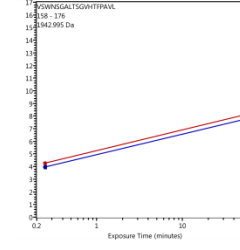
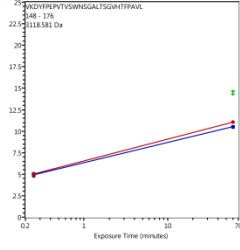
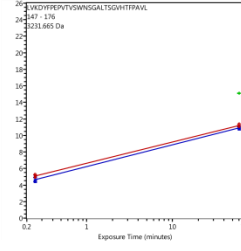
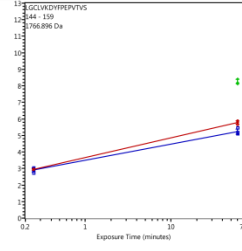
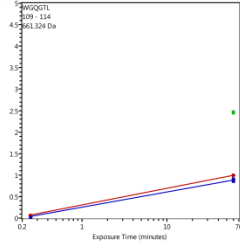
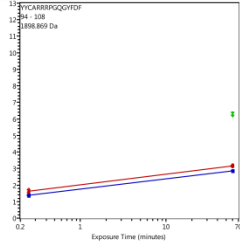
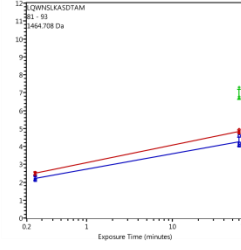
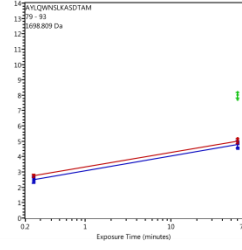
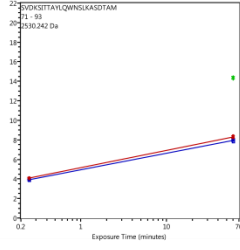
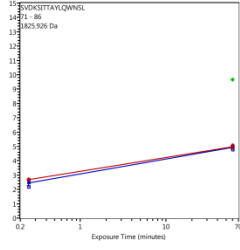
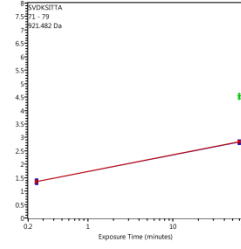
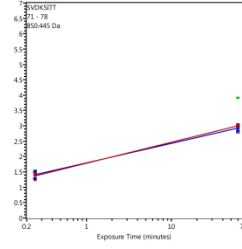
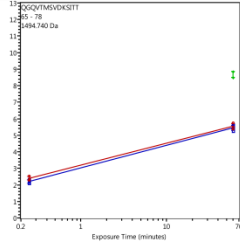
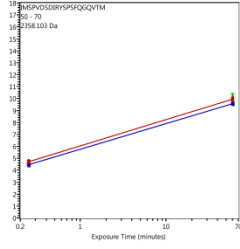
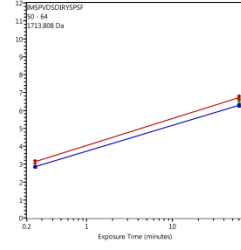
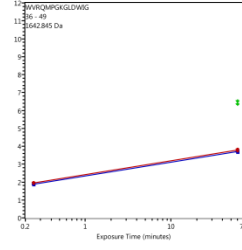
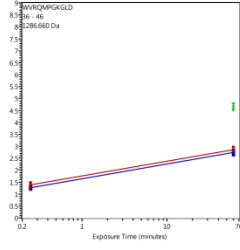
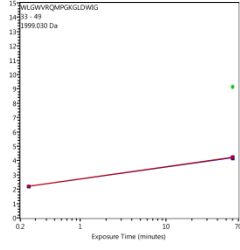
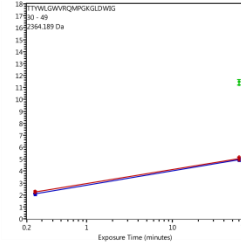
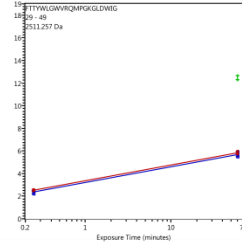
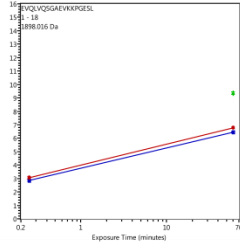
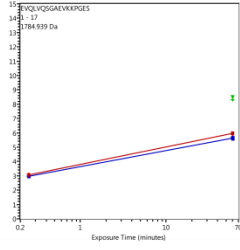




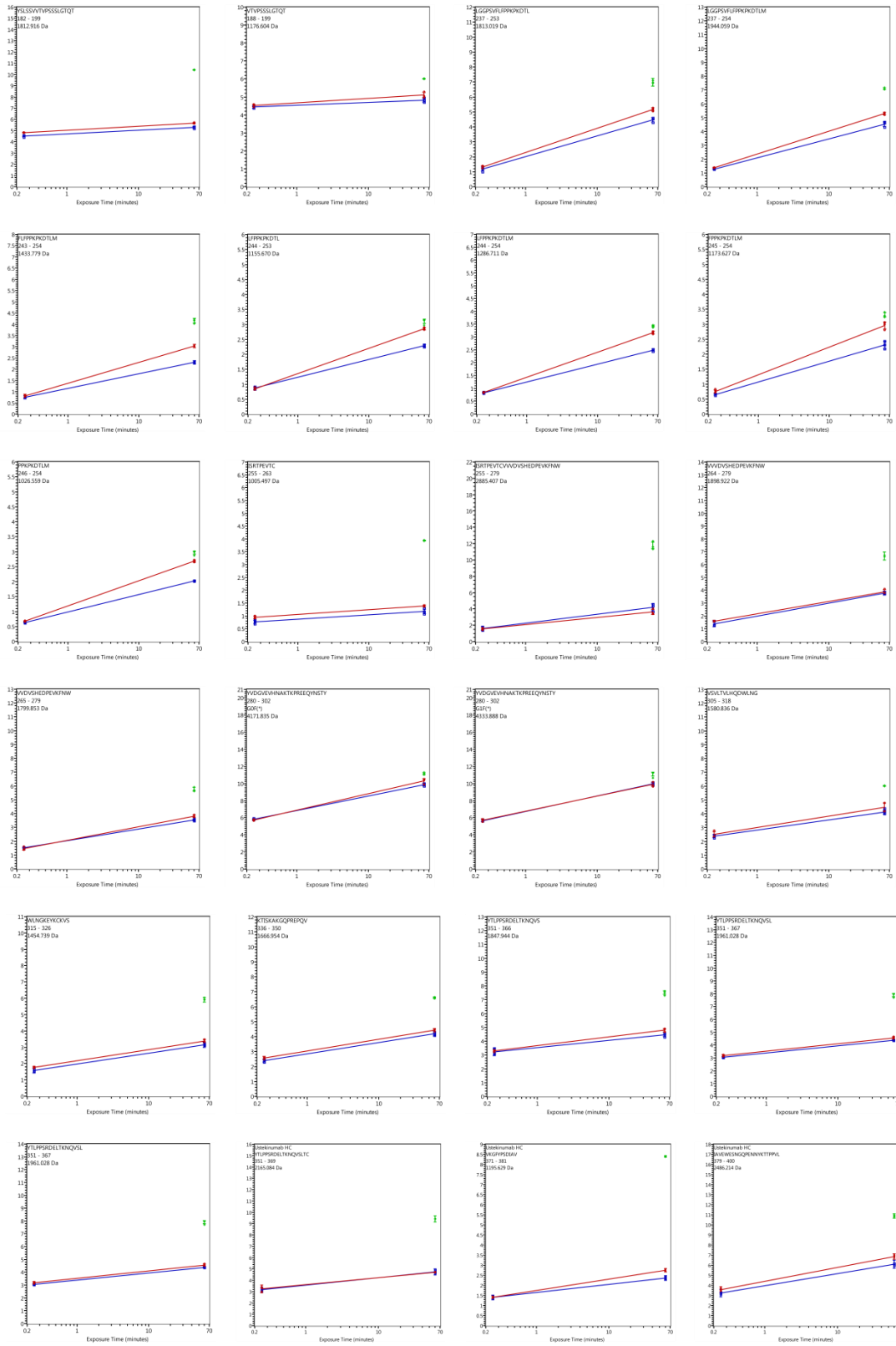
**Figure S2.** Deuterium uptake plots of light chain briakinumab and the briakinumab variant peptides. Deuterium incorporation of unbound briakinumab (red), FcRn-bound briakinumab (blue), unbound briakinumab variant (green), FcRn-bound briakinumab variant (purple) was determined in triplicate experiments at 15 s, 1 min, 1 h, 2.5 h and 5h and plotted with 1x standard deviation (in most cases the SD was lower than the size of the data point marker). The 90 % D<sub>2</sub>O control is shown in orange at the last time point.

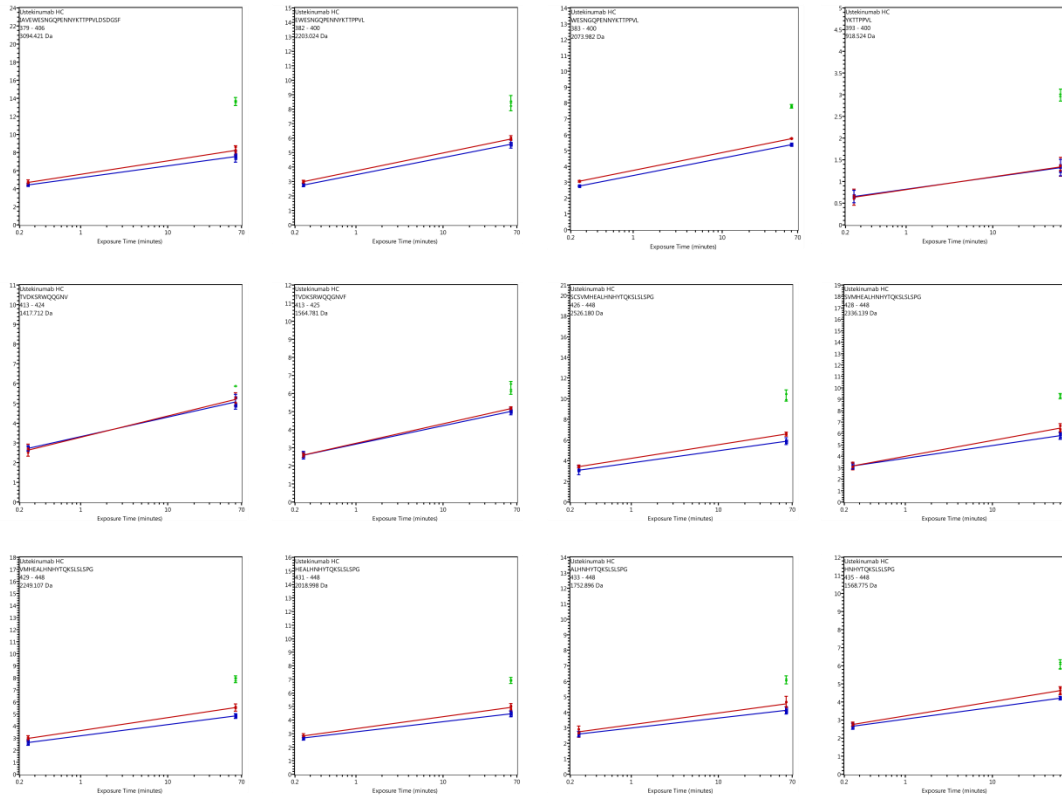


**Figure S3.** Sequence coverage map of briakinumab and the briakinumab variant A) heavy chain and B) light chain.

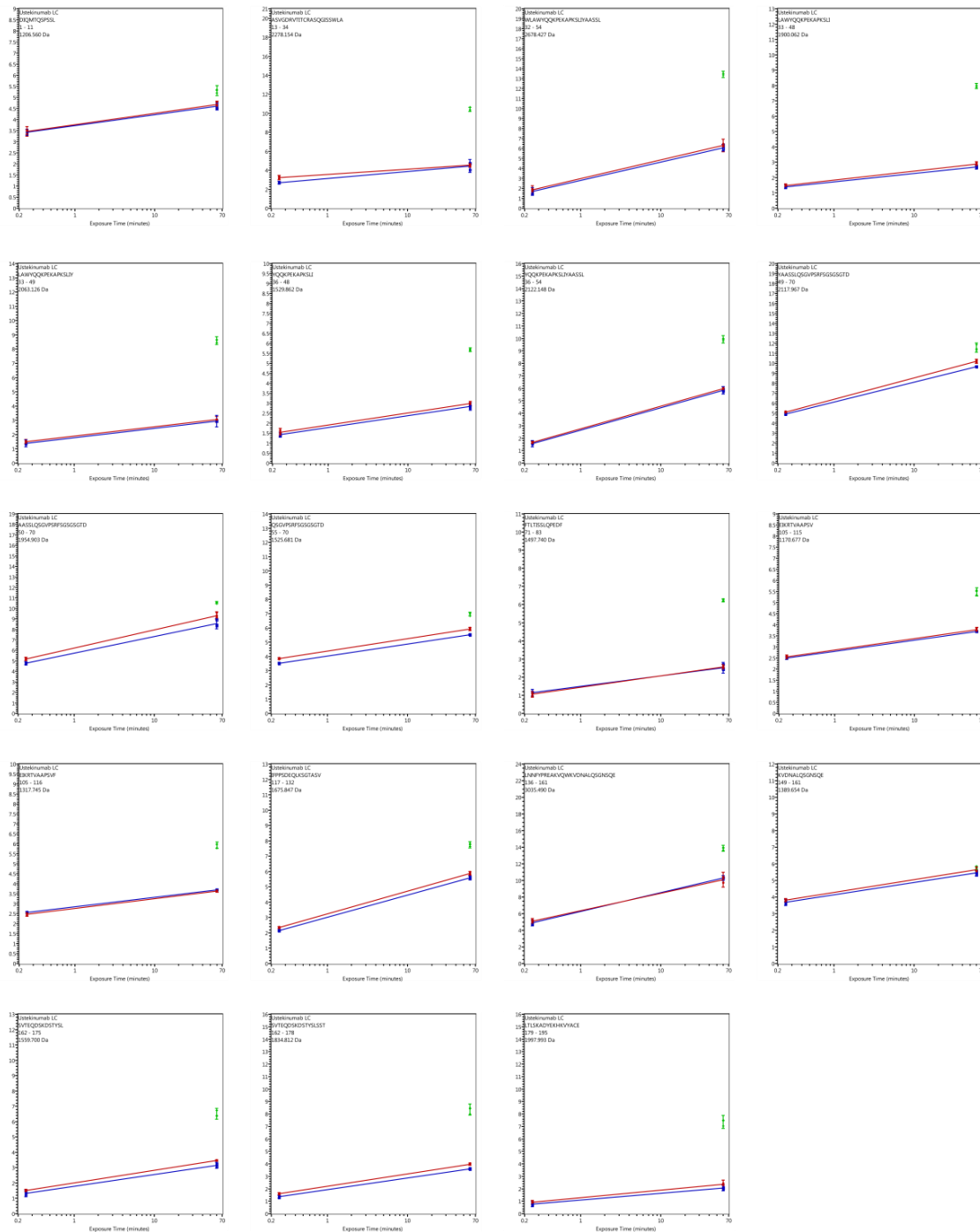








**Figure S4.** Deuterium uptake plots of heavy chain ustekinumab peptides. Deuterium incorporation of unbound ustekinumab (red), FcRn-bound ustekinumab (blue) was determined in triplicate experiments at 15 s and 1 h and plotted with 1x standard deviation (in most cases the SD was lower than the size of the data point marker). The 90 % D<sub>2</sub>O control is shown in green at the last time point.

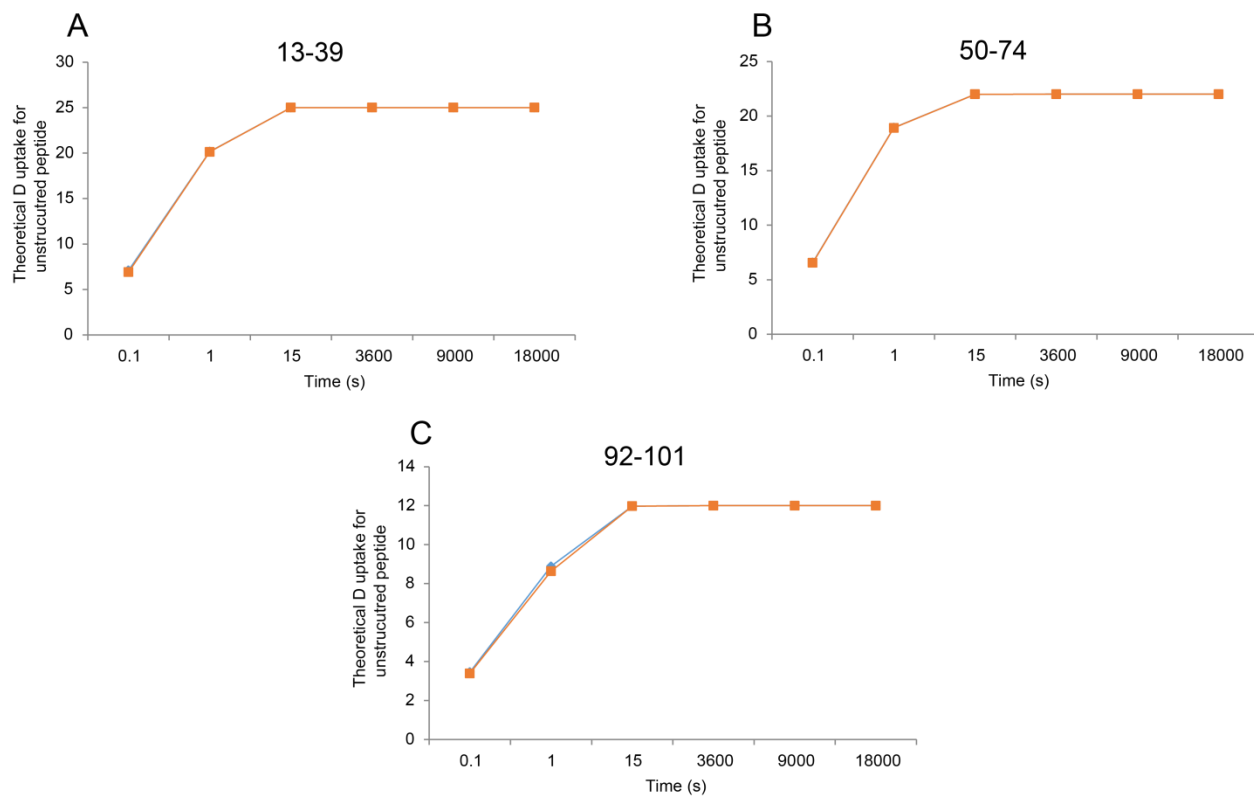


**Figure S5.** Deuterium uptake plots of light chain ustekinumab peptides. Deuterium incorporation of unbound ustekinumab (red), FcRn-bound ustekinumab (blue) was determined in triplicate experiments at 15 s and 1 h. and

plotted with 1x standard deviation (in most cases the SD was lower than the size of the data point marker). The 90 % D<sub>2</sub>O control is shown in green at the last time point.



**Figure S6.** Sequence coverage map of ustekinumab A) heavy chain and B) light chain.



**Figure S7.** Comparison of theoretical deuterium uptake of unstructured peptides of briakinumab and the briakinumab variant. Theoretical deuterium uptake of peptides containing the R to A substitution: A) 13-39, B) 50-74 and C) 92-101 of briakinumab (blue) and the briakinumab variant (orange) at time points 0.1 s, 1 s, 15 s, 1 h, 2.5 h and 5 h. The theoretical uptake for random coil peptides was calculated using intrinsic exchange rates of Bai et al. (18)

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Bria  -QSVLTQPPSVSGAPGQRVTISCSGSRSNIGSNTVKWYQQLPGTAPKLLIYYNDQRPSGV  59
Uste  DIQMTQSPSSLSASVGDRTITCRASQG--ISSWLAWYQQKPEKAPKSLIYAASSLQSGV  58
      .:  .* *:*.: *:***:* .*:  * . : **** * .*** *** .. ***

Bria  PDRFSGSKSGTSASLAITGLQAEDEADYQCQSYDRYTHPALLFGTGTKVTVLGQPKAAPS  119
Uste  PSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNIYP---YTFGQGTKLEI-KRTVAAPS  114
      *.***** ***. :*:*.** ** * *****.*: *      ** ***: : : ****

Bria  VTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPIKAGVE-TTTPSKQSNNKYA  178
Uste  VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS  174
      * :****.*:*.: .*:***:.*** ..* **.*.: .. : :.* .....*:*

Bria  ASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP-----  213
Uste  LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC  214
      ** *:*: :.:.*: *:*:***:* : * :

```

**Figure S8.** Sequence alignment of ustekinumab and briakinumab LC. Sequence alignment performed with Clustal Omega. (\*) indicates a fully conserved residue, (:) indicates conservation between residues with strongly similar properties, and (.) indicates conservation between residues with weakly similar properties. (20)